

FIGURE 1

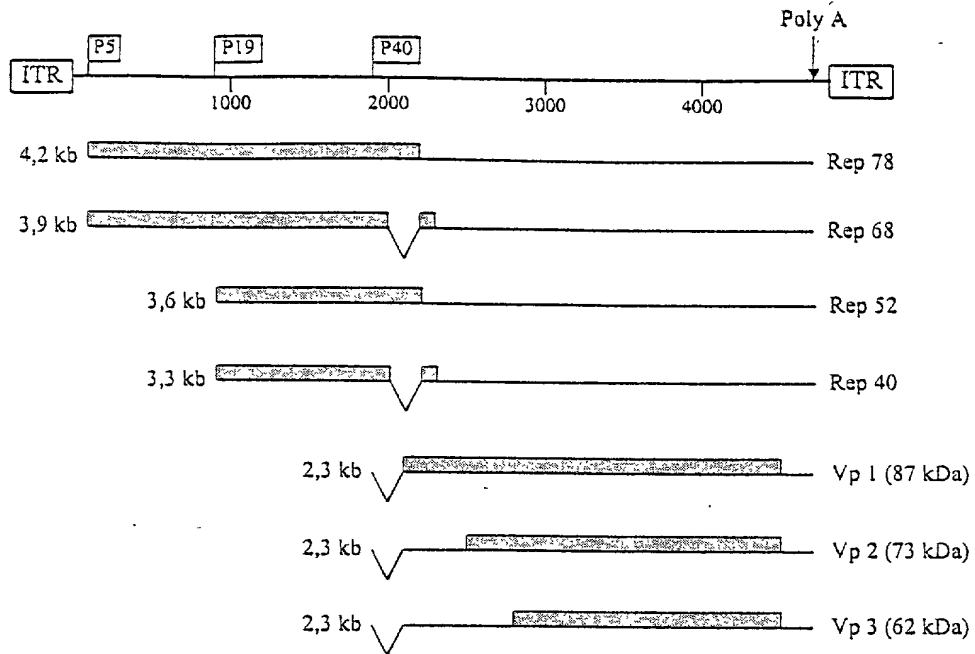


FIGURE 2A

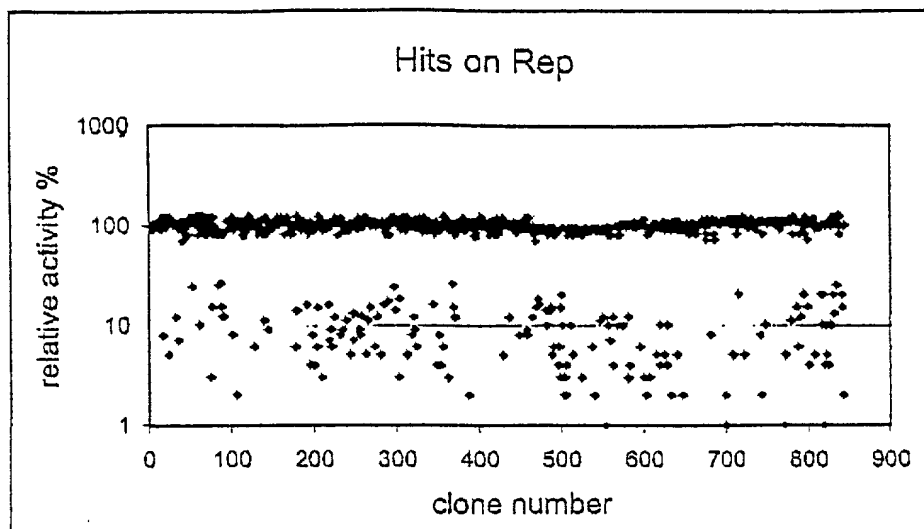


FIGURE 2B

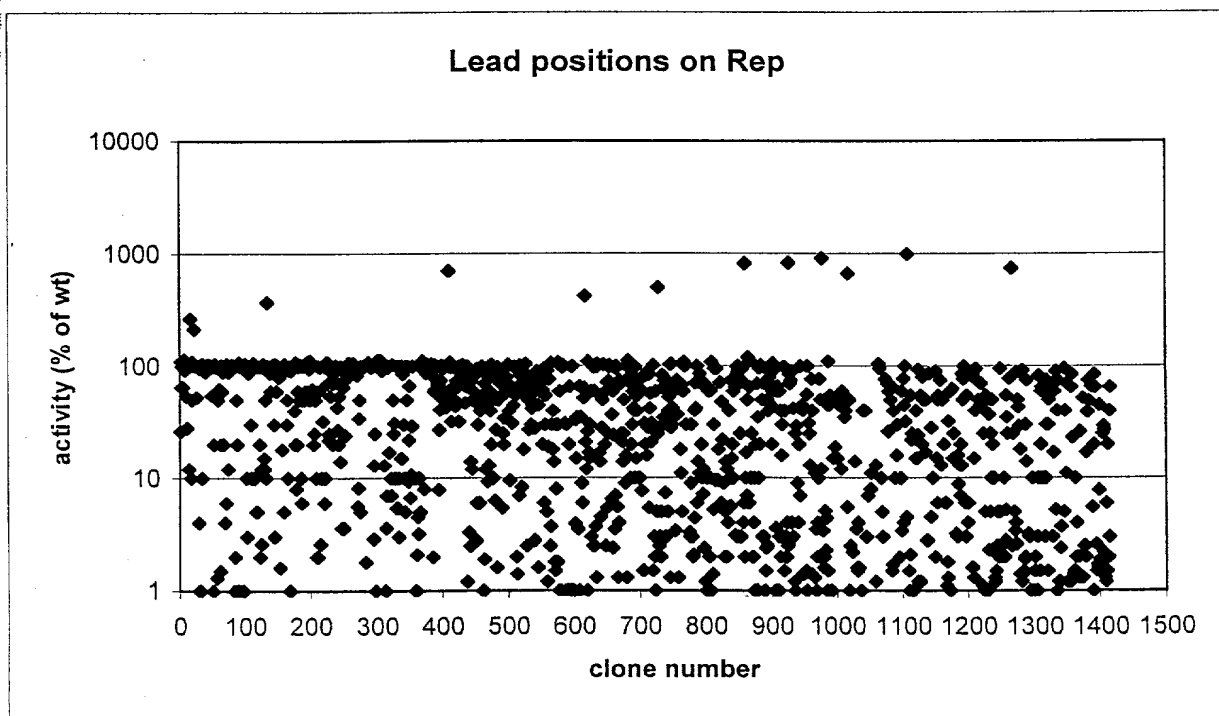


FIGURE 3A

10 20 30 40 50 60
1 MPGFYEIVIKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60
2 MPGFYEIVIKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60
3 MPGFYEIVIKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60
4 MPGFYEIVIKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60
5 MPGFYEIVIKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60
6 MPGFYEIVIKVPSDDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ 60
7 MATFYEVIVRVPFDVEEHLPGISDSFVWVTGQIWELPPESDLNLTLVEQPQLTVADRIR 60
C M**FYE**:*VP*D***HLPGIS+SFV:WV****WELPP*SD**+*L*EQ**LTVA****
70 80 90 100 110 120
1 RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHLVETTGVKSMVLGRFLSQIRDKLVTQTI 120
2 RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHLVETTGVKSMVLGRFLSQIRDKLVTQTI 120
3 REFLVEWRRVSKAPEALFFVQFEKGETYFHLHLVLIETIGVKSMVGRYVSQIKEKLVTRI 120
4 REFLVEWRRVSKAPEALFFVQFEKGETYFHLHLVLIETIGVKSMVGRYVSQIKEKLVTRI 120
5 REFLVEWRRVSKAPEALFFVQFEKGDYFHLHLVETVGVKSMVGRYVSQIKEKLVTRI 120
6 RDFLTEWRRVSKAPEALFFVQFEKGESYFHMHLVETTGVKSMVLGRFLSQIREKLIQRI 120
7 RVFLYEWNKFSKQ-ESKFFVQFEKGESYFHLHLVETSGISSMVLGRYVSQIRAQLVKVV 119
C R:FL++W***SK**E***FFVQFEKG+:YFH*H:L+ET:G**SMV:GR::SQI::*L*:::
130 140 150 160 170 180
1 YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEEYISACL 180
2 YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEEYISACL 180
3 YRGVPEQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL 180
4 YRGVPEQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL 180
5 YRGVPEQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYISACL 180
6 YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEQYLSACL 180
7 FQGIPEQINDVVAITKVKK--GGANKVVDSGYIPAYLLPKVQPELQWAWTNLDEYKLAAL 177
C **G:EP:***W*A*TK****GG*NKVD:*YIP*YLLPK*QPELQWAWTN*:Y:*A*L
190 200 210 220 230 240
1 NLAERKRLVAQHLTHVSQTQEONKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240
2 NLAERKRLVAHDLTHVSQTQEONKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240
3 NLAERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240
4 NLAERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240
5 NLAERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK 240
6 NLTERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKTSARYMELVGWLVDKGITSEK 240
7 NLEERKRLVAQFLAESSQRS-QEASQREFSADPVIKSKTSQKYMALVNVLVEHGITSEK 236
C NL+ERKRLVA*+L***SQ***Q****+***S**PVI*SKTS**YM*LV*WLV*+GITSEK
250 260 270 280 290 300
1 QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPPADIKTNRIYR 300
2 QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPPADIKTNRIYR 300
3 QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ 300
4 QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ 300
5 QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGQNPPEISSNRIYR 300
6 QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMSLTKTAPDYLVGQPPVEDISSNRIYK 300
7 QWIQENQESYLSFNSTGNSRSQIKAALDNATKIMSLTKSAVDYLVGSSVPEDISKNIWQ 296
C QWIQE*Q*SY*SFN***NSRSQIKAALDNA:KIM+LTK:A*DYLVG::**+DI::NRI*:
310 320 330 340 350 360
1 ILELNGYEPAYAGSVFLGWAQKRFGKRNTIWLFGPATTGKTNIAEAIHAHVPFYGCVNWT 360
2 ILELNGYDPAYAGSVFLGWAQKRFGKRNTIWLFGPATTGKTNIAEAIHAHVPFYGCVNWT 360
3 ILELNGYDPQYAAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIHAHVPFYGCVNWT 360
4 ILELNGYDPQYAAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIHAHVPFYGCVNWT 360
5 ILELNGYDPQYAAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIHAHVPFYGCVNWT 360
6 ILELNGYDPQYAAASVFLGWATKKFGKRNTIWLFGPATTGKTNIAEAIHAHVPFYGCVNWT 360
7 IFEMNGYDPAYAGSILYGWCQRSFNKRNTVWLYGPATTGKTNIAEAIHAHVPFYGCVNWT 356
C I*E+NGY*P:YA:S***GW***:F*KRNT*WL*GPATTGKTNIAEAIHAH+VPFYGCVNWT

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FIGURE 3B

	370	380	390	400	410	420	
1	NENFPFNDCVDK	MVIWWEEGKMTAKV	VE	SAKAILGGSKVR	VDQKCKSSAQIDPT	TPVIVTS	420
2	NENFPFNDCVDK	MVIWWEEGKMTAKV	VE	SAKAILGGSKVR	VDQKCKSSAQIDPT	TPVIVTS	420
3	NENFPFNDCVDK	MVIWWEEGKMTAKV	VE	SAKAILGGSKVR	VDQKCKSSAQIEPT	TPVIVTS	420
4	NENFPFNDCVDK	MVIWWEEGKMTAKV	VE	SAKAILGGSKVR	VDQKCKSSAQIEPT	TPVIVTS	420
5	NENFPFNDCVDK	MVIWWEEGKMTAKV	VE	SAKAILGGSKVR	VDQKCKSSAQIDPT	TPVIVTS	420
6	NENFPFNDCVDK	MVIWWEEGKMTAKV	VE	SAKAILGGSKVR	VDQKCKSSAQIDPT	TPVIVTS	420
7	NENFPFNDCVDK	MLIWWEEGKMTINKV	VE	SAKAILGGSKVR	VDQKCKSSVQIDST	TPVIVTS	416
C	NENFPFNDCVDK	M*IWWEEGKMT*KV	VE	SAKAILGGSKVR	VDQKCKSS*QI+*TP	TPVIVTS	
	430	440	450	460	470	480	
1	NTNMC	CAVIDG	NSTT	FEHQOPLQDRM	FKFELTRRLEHDFG	KVTKQEVKEFFR	WAQD
2	NTNMC	CAVIDG	NSTT	FEHQOPLQDRM	FKFELTRRLEHDFG	KVTKQEVKEFFR	WAQD
3	NTNMC	CAVIDG	NSTT	FEHQOPLQDRM	FKFELTRRLDHD	FGKVTQEVKDF	FRWASDHVTDV
4	NTNMC	CAVIDG	NSTT	FEHQOPLQDRM	FKFELTRRLDHD	FGKVTQEVKDF	FRWASDHVTDV
5	NTNMC	CAVIDG	NSTT	FEHQOPLQDRM	FKFELTKRLEHDFG	KVTKQEVKDF	FRWASDHVTEV
6	NTNMC	CAVIDG	NSTT	FEHQOPLQDRM	FKFELTRRLDHD	FGKVTQEVKDF	FRWAKDHVVEV
7	NTNMC	CVVDG	NSTT	FEHQOPLQDRM	FKFELTKRLPPD	FGKITKQEVKDF	FAWAKVNQVPV
C	NTNMC	*V*DG	NSTT	FEHQOPL*DRM	FKFELT+RL:*	DFGK*TKQEVK+FF*WA:***+:V	
	490	500		510	520		
1	AHEFYVRKGG	GANKRPAPDDADK	SEPKRA-----	CPSVADP	STSDAEG		522
2	AHEFYVRKGG	GANKRPAPDDADK	SEPKRA-----	CPSVADP	STSDAEG		522
3	AHEFYVRKGG	AKKR	PASNDADVSEPKRQ-----	CTSLAQPT	TTSDAEA		522
4	AHEFYVRKGG	AKKR	PASNDADVSEPKRQ-----	CTSLAQPT	TTSDAEA		522
5	THEFYVRKGG	AKKR	PAPNDADISEPKRA-----	CPSVAQP	STSDAEA		522
6	EHEFYVRKGG	AKKR	PAPSDADISEPKRV-----	RESVAQP	STSDAEA		522
7	THEFKVP	PRELAGTKGA	EKSLKRPLGDVNTS	YKSLEKRARLS	FVPETPRSSDV	TVPAPL	536
C	:HEF	*V+***A:***A:***:*****:				+*:*:*:***A*:	
	530	540	550	560	570	580	
1	APVDFADRYQ	NKCSRHAGMLQMLF	PCKTCERMNQ	NFNICFTHGTRD	CSECFP--GV	SESEQ	580
2	APVDFADRYQ	NKCSRHAGMLQMLF	PCKTCERMNQ	NFNICFTHGTRD	CSECFP--GV	SESEQ	580
3	P-ADYADRYQ	NKCSRHVGMN	LMLFPCKTCERMN	QISNVCFTHGQRD	CGECFPGMS	ESQPV	581
4	P-ADYADRYQ	NKCSRHVGMN	LMLFPCKTCERMN	QISNVCFTHGQRD	CGECFPGMS	ESQPV	581
5	P-VDYADRYQ	NKCSRHVGMN	LMLFPCKTCERMN	QNVDFTHGVMDC	AEACFP--V	SESQPV	580
6	S-INYADRYQ	NKCSRHVGMN	LMLFPCKTCERMN	QNSNICFTHGQK	DCLECFP--V	SESQPV	579
7	RPLNWN	SRDYDCKDYHAQFD	NI	SNKCDECEYLNRG	KNGCICHNVTHC	QICHG-----	588
C	::+:**RY**K	*C**H:***:****C::CE**N*:::C**H*:::C.*C**...+::::					
	590	600	610	620			
1	PVVRKRTYR	KLCAIHLLGRAPE	IIACSACDLVN	VDLDDCVSEQ			623
2	PVVRKRTYR	KLCAIHLLGRAPE	IIACSACDLVN	VDLDDCVSEQ			623
3	SVVKKKTYQ	KLCP	IIHILGRAPE	IIACSACDLAN	VDLDDCVSEQ		624
4	SVVKKKTYQ	KLCP	IIHILGRAPE	IIACSACDLAN	VDLDDCVSEQ		624
5	SVVRKRTYQ	KLCP	IIHIMGRAPE	VACSACELAN	VDLDDCDMEQ		623
6	VSVVKKAYQ	KL	CIYIHHIMG-KVP	DACTACDLVN	VDLDDCIFEQ		621
7	-----						
C	+++::**RY**K	*C**H:***:****C::CE**N*:::C**H*:::C.*C**...+::::					